

Table IV. HLA Class I Standard Peptide Binding Affinity.

M3	

ALLELE	STANDARD	SEQUENCE	SEQ ID NO:	STANDARD
	PEPTIDE			BINDING AFFINITY
		4		(nM)
A*0101	944.02	YLEPAIAKY	1189	25
A*0201	941.01	FLPSDYFPSV	1190	5.0
A*0202	941.01	FLPSDYFPSV	1191	4.3
A*0203	941.01	FLPSDYFPSV	1192	10
A*0205	941.01	FLPSDYFPSV	1193	4.3
A*0206	941.01	FLPSDYFPSV	1194	3.7
A*0207	941.01	FLPSDYFPSV	1195	23
A*6802	1072.34	YVIKVSARV	1196	8.0
A*0301	941.12	KVFPYALINK	1197	11
A*1101	940.06	AVDLYHFLK	1198	6.0
A*3101	941.12	KVFPYALINK	1199	18
A*3301	1083.02	STLPETYVVRR	1200	29
A*6801	941.12	KVFPYALINK	1201	8.0
A*2402	979.02	AYIDNYNKF	1202	12
B*0702	1075.23	APRTLVYLL	1203	5.5
B*3501	1021.05	FPFKYAAAF	1204	7.2
B51	1021.05	FPFKYAAAF	1205	5.5
B*5301	1021.05	FPFKYAAAF	1206	9.3
B*5401	1021.05	FPFKYAAAF	1207	10



Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard	Sequence	SEQ	Binding
		Peptide		ID	Affinity
				NO:	(nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2β1	507.02	GRTQDENPVVHFFKNIVTP	1220	9.1
			RTPPP		
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	1222	58
DRB5*0101	DR2w2β2	553.01	QYIKANSKFIGITE	1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

as

61340	DRSWLZ																																								
7	DKSWII												0.2000						0.0080																						
7	UK4WI5																																								
ing Data	DK4W4						-0.0027						8.3000				1000	-0.002/	0.0560		2000	700.0									0.0100										
with Bindi	DK3						,	0.0150	0,000	600.0			0.0027						9000.0		0.0030				0.0380	0.0300										-0.0025					
Super Motif Peptides with Binding Data	DK2W2B2												0.1200						0.0370																						
uper Moti	DK2wist												0.0360	;					0.0016																						
	UKI						0.0400						1.9000				2000	-0.0003	0.2500		5000	200.0									0.0010										
	Position	119	347	2 5	S &	229	324	45	7	% % %	134	19	108	296 296	214	233	S S	ςς: - Ε	130	32	252	169	345	53	47	142	4	110	267	249	248	569	197	33	8	215	2 2	203	143 217	23	234
Table XIX	Exemplary SeqID Num	1057	1058	1059	1061	1062	1063	1064	1065	1060	1068	1069	1070	1071	1073	1074	1075	10/0	1078	1079	1080	1082	1083	1084	1085	1080	1088	1089	1090	1091	1093	1094	260	1097	1098	1099	1101	1102	1103		1106
	Exemplary Sequence	AKSVTCTYSPALNKM	ALELKDAQAGKEPGG	APPVAPAPAAPTPAA	APKWPEAAFFVAFAF APSWPLSSSVPSOKT	CTTIHYNYMCNSSCM	JGEYFTLQIRGRERF	DLMLSPDDIEQWFTE	OPSVEPPLSQETFSD	SGNLKVEYLDDKNIF	SCOLAKTCPVOLWVD	SDLWKLLPENNVLS	GFRLGFLHSGTAKSV	GTRVRAMALYKUSQH HHEI PPGSTKRAI PN	HSVVVPYEPPEVGSD	HYNYMCNSSCMGGMN	EQWFTEDPGPDEAP	KRALPNNISSSPOPK	LNKMFCOLAKTCPVQ	SPLPSQAMDDLMLS	LTIITLEDSSGNLLG	MITEVVRRCPHHERCS	NEALELKDAQAGKEP	NNVLSPLPSQAMDDL	PDDIEQWFTEDPGPD	PPEVGSDC11IHYNY DVOI WVDSTPPPGTR	OLWVDSTPPPGTRVR	RLGFLHSGTAKSVTC	RNSFEVRVCACPGRD	KNIFKHSVVVFIEFF RPII TIITI FINSKA	RRPILTITLEDSSG	SFEVRVCACPGRDRR	SGNLLGRNSFEVRVC	SOAMDDLMLSPDDIE	SSSVPSQKTYQGSYG	SVVVPYEPPEVGSDC	SWFLSSSVFSQN11Q SVGFR1GF1HSGTAK	VEYLDDRNTFRHSVV	VQLWVDSTPPPGTRV	WKLLPENNVLSPLPS	YNYMCNSSCMGGMNR
	Core SeqID Num	1123 AK	4	1125 AP	1126 AF	,	, I	1130 DL	1131 DP	1132 EC	1133 EN			1137 GI	_	_			1145 1144 LN			1147 MR		. 0	1151 PC	1152 Pt	1154	1155 RI	1156 RJ	1157 KJ				162 Sr 1163 SC			1166 57		V 6911	1171	1172 Y
	Core Sequence	VTCTYSPAL	LKDAQAGKE	VAPAPAAPT	MPEAAPPVA WPI SSSVPS	HYNYMCNS	YFTLQIRGR	LSPDDIEQW	VEPPLSQET	LRVEYLDDR	VLSFLFSQA	LWKLLPENN	LGFLHSGTA	VRAMAIYKQ 1 pbcstrpa	VVPYEPPEV	YMCNSSCMG	WFTEDPGPD	LPNNTSSSP	MFCOLAKTC	LPSQAMDDL	ITLEDSSGN	MNKKFILII	LELKDAOAG	LSPLPSQAM	IEQWFTEDP	VGSDCTITH	VDSTPPPGT	FLHSGTAKS	FEVRVCACP	FRHSVVVPY	LTITLED	VRVCACPGR	LLGRNSFEV	LNKMFCQLA MDDI MI SPD	VPSQKTYQG	VPYEPPEVG	ESSSVPSQK	LDDRNTFRH	WVDSTPPPG	LPENNVLSP	MCNSSCMGG

	DRw53						
	DR9						
£2 DD C Motif Dentides with Rinding Data	DR8w2		1.7000	0.0320			
antidos wit	epuldes wil	-0.0018	0.2800	-0.0007	-0.0007	0.0023	
Cunor Motif D	Super Mount		0.0460	9600.0			
T. 2. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	Exemplary SeqID Num	1058 1058 1060 1061 1063 1065 1066	1068 1069 1070 1072 1073	1074 1075 1076 1077 1078	1080 1081 1082 1083	1085 1086 1087 1089 1090 1094 1095 1096	1099 1100 1103 1104 1105
W.t.l. VIV	Exemplary Sequence	AKSVTCTYSPALNKM ALELKDAQAGKEPGG APPVAPAPAAPTPAA APRMPEAAPPVAPAP APSWPLSSSVPSQKT CTTIHYNYMCNSSCM DGEYFTLQIRGRERF DLMLSPDDIEQWFTE DPSVEPPLSQETFSD EGNLRVEYLDDRNTF	ENNYLSPLPSQAMDD FCQLAKTCPVQLWVD FSDLWKLLPENNVLS GFRLGFLHSGTAKSV GTRVRAMAIYKQSQH HHELPPGSTKRALPN HSVVVPVFPPFVGSD	HYNYMCNSSCMGGMN IEQWFTEDPGPDEAP KRALPNNTSSSPQPK LGFLHSGTAKSVTCT LNKMFCQLAKTCPVQ	LYLLY SQAMDDEMES LTIITLEDSSGNLLG MGGMNRRPILTIITL MTEVVRRCPHHERCS NFALELKDAOAGKEP	NNVLSPLPSQAMDDL PDDIEQWFTEDPGPD PPEVGSDCTTIHYNY PVQLWVDSTPPPGTR QLWVDSTPPPGTR QLWVDSTPPPGTR RLGFLHSGTAKSVTC RNSFEVRVCACPGRD RNTFRHSVVVPYEPP RPILTITLEDSSGN RRPILTITLEDSSG SFEVRVCACPGRDRR SGNLLGRNSFEVRVC SQAMDDLMLSPDDIE SSCVPSOKTYOGSYG	SVVVPYEPPEVGSDC SWPLSSSVPSQKTYQ SYGFRLGFLHSGTAK VEYLDDRNTFRHSVV VQLWVDSTPPPGTRV VVPYEPPEVGSDCTT WKLLPENNVLSPLPS
	Core SeqID Num	1123 1124 1125 1127 1129 1130	1135 1135 1136 1137 1138	1140 1141 1143 1144	1146 1146 1147 1148	1150 1151 1153 1154 1156 1160 1161 1163	1165 1166 1167 1168 1169 1170 1171
	Core	VTCTYSPAL LKDAQAGKE VAPAPAPT MPEAAPPVA WPLSSSVPS IHYNYMCNS YFTLQIRGR LSPDDIEQW VEPPLSQET LRVEYLDDR	VLSPLPSQA LAKTCPVQL LWKLLPENN LGFLHSGTA VRAMAIYKQ LPPGSTKRA	YMCNSSCMG WFTEDPGPD LPNNTSSSP LHSGTAKSV MFCQLAKTC	LPSQAMDDL ITLEDSSGN MNRRPILTI VVRRCPHHE	LSPLPSQAM IEQWFTEDP VGSDCTTIH LWVDSTPPPF VDSTPPPGT FLHSGTAKS FEVRVCACP FRHSVVVPY LTIITLED VRVCACPGR LLGRNSFEV LLGRNSFEV LNKMFCQLA MDDLMLSPD	VPYEPPEVG LSSSVPSQK FRLGFLHSG LDDRNTFRH WVDSTPPPG YEPPEVGSD LPENNVLSP MCNSSCMGG

DRWS3

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					Table XXa		3a Motif	p53 DR 3a Motif Peptides with Binding Data	ing Data		
Core	Core SeqID	Exemplary Sequence	Exemplary SeqID Num.	Position	DR1	DR2w2B1 DR2w2B2	S DR3	DR4w4	DR4w15	DR5w11	DR5w12
Salanhac	Timer		4								
LSPDDIEOW	1173	DLMLSPDDIEQWFTE	1107	42			0.0150	0			
LRVEYLDDR	1174	EGNLRVEYLDDRNTF	1108	198			0.0039	6			
LSOETFSDL	1175	EPPLSOETFSDLWKL	1109	11			-0.0025	Š			
FTEDPGPDE	1176	EOWFTEDPGPDEAPR	1110	51			-0.002	5			
LDGEYFTLO	1177	KKPLDGEYFTLQIRG	_	320			-0.002	5			
ITLEDSSGN	1178	LTHTLEDSSGNLLG	_	252			0.003	0			
LLPENNVLS	1179	LWKLLPENNVLSPLP	_	77			0.002	6			
VGSDCTTIH	1180	PPEVGSDCTTIHYNY	1114	222			0.0380	0			
LWVDSTPPP	1181	PVOLWVDSTPPPGTR	_	142			0.030	9			
IRVEGNLRV	1182	OHLIRVEGNLRVEYL	_	192			0960'0	0			
MFRELNEAL		RFEMFRELNEALELK	1117	337			0.0052	.5			
YLDDRNTFR	1184	RVEYLDDRNTFRHSV	_	202			0.180	<u>o</u>			
VPVFPPFVG	-	SVVVPYEPPEVGSDC	1119	215			-0.0025	ξ .			

65	1
don	
	w53

ABNI	18	
	DR5w12	
	DR5w11	
ling Data	DR4w15 DR5w11	
with Bind	DR4w4	
f Peptides	DR3	0.0290 0.0930 -0.0025
p53 DR 3b Motif Peptides with Binding Data	DR2w2ß2	
	DR2w281	
Table XXb	DR1	
	Position	325 194 160
	Exemplary SeqID Num	1120 1121 1122
	Exemplary Sequence	GEYFTLQIRGRERFE LIRVEGNLRVEYLDD MAIYKQSQHMTEVVR
	Core SeqID Num	1186 G 1187 L 1188 M
	Core	FTLQIRGRE VEGNLRVEY YKQSQHMTE

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CON	lude

			dr.I.	Table XXb	t and eed	pss DR so Motif Feptides with Dilluing Data	es with Dill	uiig Data	
Core Sequence	Core SeqID Num	Core SeqID Exemplary Num Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53	
FTLQIRGRE VEGNLRVEY VKOSOHMTE	1186	GEYFTLQIRGRERFE LIRVEGNLRVEYLDD MAIYKOSOHMTEVVR	1120 1121 1122						

Table XXII. A2 supermotif analogs

6			SEQ	A*0201
Source	AA	Sequence	ID NO:	nM
p53.24	9	KLLPENNVL	NO:	212
p53.24V9	9	KLLPENNVV	1224	313
•	_		1225	385
p53.25	11	LLPENNVLSPL	1226	19
p53.25V9	11	LLPENNVLSPV	1227	39
p53.65	9	RMPEAAPPV	1228	119
p53.65L2	9	RLPEAAPPV	1229	78 7 8
p53.65	10	RMPEAAPPVA	1230	78
p53.65L2V10	10	RLPEAAPPVV	1231	143
p53.65M2V10	10	RMPEAAPPVV	1232	54
p53.69	8	AAPPVAPA	1233	5000
p53.69L2V8	8	ALPPVAPV	1234	217
p53.101	11	KTYQGSYGFRL	1235	1786
p53.101L2V11	11	KLYQGSYGFRV	1236	81
p53.113	11	FLHSGTAKSVT	1237	5000
p53.113V11	11	FLHSGTAKSVV	1238	1220
p53.129	9	ALNKMFCQL	1239	735
p53.129V9	9	ALNKMFCQV	1240	75
p53.129B7V9	9	ALNKMFBQV	1241	192
p53.129	10	ALNKMFCQLA	1242	1316
p53.129V10	10	ALNKMFCQLV	1243	217
p53.132	9	KMFCQLAKT	1244	333
p53.132V9	9	KMFCQLAKV	1245	33
p53.132B4V9	9	KMFBQLAKV	1246	125
p53.132L2V9	9	KLFCQLAKV	1247	98
p53.135	9	CQLAKTCPV	1248	208
p53.135L2	. 9	CLLAKTCPV	1249	125
p53.135B1B7	9	BQLAKTBPV	1250	102
p53.135B1L2B7	9	BLLAKTBPV	1251	46
p53.139	9	KTCPVQLWV	1252	725
p53.139L2	9	KLCPVQLWV	1252	122
p53.139L2B3	9	KLBPVQLWV	1253	46
p53.149	<u>9</u>	STPPPGTRV	1 -	
p53.149M2	9		1255	909
p53.149L2	9	SMPPPGTRV	1256	172
p53.149L2	9	SLPPPGTRV	1257	122
	9	KQSQHMTEV	1258	500
p53.164L2		KLSQHMTEV	1259	122
p53.216	10	VVVPYEPPEV	1260	617
p53.216L2	10	VLVPYEPPEV	1261	89
p53.229	9	CTTIHYNYM	1262	278
p53.229L2V9	9	CLTIHYNYV	1263	263
o53.229B1L2V9	9	BLTIHYNYV	1264	116
p53.236	8	YMCNSSCM	1265	4546
53.236L2M8	8	YLCNSSCV	1266	
553.236	11	YMCNSSCMGGM	1267	667
53.236L2M11	11	YLCNSSCMGGV	1268	22
53.255	11	ITLEDSSGNLL	1269	1563
o53.255L2V11	11	ILLEDSSGNLV	1270	33
53.256	10	TLEDSSGNLL	1271	1667
o53.256V10	10	TLEDSSGNLV	1272	4167

Table XXIIA A01 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	<u>A*0101 nM</u>
52.0136	11	GSDCTTIHYNY	1273	p53.226	67.6
57.0035	9	GTDCTTIHY	1274	p53.226.T2	0.9
57.0125	10	PTQKTYQGSY	1275	p53.98.T2	35.7
57.0126	10	GTDKSVTCTY	1276	p53.117.D3	42.4
57.0127	10	RVDGNLRVEY	1277	p53.196.D3	45.5



Table XXIIB A03 Analog Peptides

A3 XRN	4	. 4	. 4	ى -) 	က	· m	· ~) (C)) 4	. ~	۱ ۵	ı က	· സ
A*6801 nM A		38.1	500	14.8	8888.9	13333.3	666.7	29.6	17		4.11	2500	1509.4	200
A*3301 nM	10000	-72500	22307.7	85,3	-72500	-72500	138.1	-72500	-72500	852.9	805.6	-72500	18125	1381
A*3101 nM	72	138.5	439	33.3	7500	418.6	8.6	0006	-36000	120	620.7	4615.4	295.1	183.7
A*1101 nM	61.9		12.8	8.3	461.5	136.4	1666.7	17.1	75	95.2	25	200	54.5	2857.1
A*0301 nM /	37.9	33.3	15.7	25	846.2	57.9	40.7	12.5	100	161.8	1000	314.3	33.3	196.4
Source	p53.101.V2	p53.101.V2K10	p53.124.B1V2	p53.124.B1V2R9	p53.132.V2B4	p53.154.V2	p53.156.R9	p53.240.V2B3K9	p53.240.V2B3K10	p53.240.V2B3	p53.240.V2B3	p53.273.B3B5K11	p53.376.V2	p53.376.V2R11
SEQ ID NO:	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291
Sednence	KVYQGSYGFR	KVYQGSYGFK	BVYSPALNK	BVYSPALNR	KVFBQLAK	GVRVRAMAIYK	RVRAMAIYR	SVBMGGMNK	SVBMGGMNRK	SVBMGGMNR	SVBMGGMNRR	RVBABPGRDRK	SVSRHKKLMFK	SVSRHKKLMFR
≸	9	10	တ	6	ω	7	တ	တ	9	တ	9	7	7	_
Peptide	1371.14	1371.15	1371.16	1371.17	1371.18	1371.2	1371.22	1371.24	1371.25	1371.26	1371.27	1371.31	1371.32	1371.33

Table XXIIC A02 Analog Peptides

A2 XRN	က		c	၇	4	-	4	. (n	•	_	~	,
A*6802 nM	-40000			-80000	20000		-80000		181.8	0000	00000-	00008	00000
			L ((7.5	1057	2.00	284 G	5:107	560.6	L 0077	1193.5	ACOL	4023
A*0203 nM A*0206 nM	19.6			18.5	17 E	C: /	160 5	2.5	2564.1		12500	U 77	C.4.
1*0202 nM	14.3			390.9	7 00	.00.	120.2	20.00	7867		1954.5	71	1/9.2
A*0201 nM		41.7	27.8	735.3		333.3	003	000	277.8	2	312.5) (35/.1
		mp53.261	mp53.261	n53,129		p53.132	7070	pp3.104	n52 220	D22.653	n53 24	1 .	p53.113
SEO ID NO:	1292	1293	1294	1295	007	1296	1000	1297	1200	0671	1299	- 200	1300
Sections	KMFCQLAKT	LLGRDSFEV	LLGRDSFEV	NKMECOI		KMECCI AKH		KOSOHMTEV		CHILLYNAM	Z DENINIVI		FLHSGTAKSV
	[ြတ												
Dontido	27 0068	39.0074	44.0003	4047.00	1317.22	1217 02	62.7161	1324 08	00:100	1329.04	70000	1329.07	1329 09

Table XXIID A24 Analog Peptides

Peptide Peptide	AA	Sequence	SEQ ID NO:	<u>Source</u>	<u>A*2401 nM</u>
52.008	8	TYQGSYGF	1301	p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0081	10	TYQGSYGFRL	1303	p53.102	100
52.0103	10	TYSPALNKMF	1304	p53.125	2.4
52.0104 52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0144 52.0147	11	TYLWWVNGQSL	1306	CEA.531	92.3
57.0042	9	LYWVNGQSF	1307	CEA.533.Y2F9	15.8
57.0042 57.0051	9	EYVNARHCF	1308	Her2/neu.553.F9	150
57.0031	9	TYSDLWKLF	1309	p53.18.Y2F9	5.5
-	9	SYGFRLGFF	1310	p53.106.F9	121.2
57.0071	10	TYQGSYGFRF	1311	p53.102.F10	30
57.0096	10	1100010111	.5	L	

Alg.

TABLE XXIIE B07 Analog Peptides

B7 XRN - 2 - 1 - 1
8*5401 nM 3846.2 500 2439 -20000 16666.7
B*5301 nM 6200 7750 23250 -23250 -31000
B*5101 nM B*5 18333.3 5500 662.7 6111.1 -55000
8*3501 nM 3000 2482.8 -36000 -24000 -36000
B*0702 nM 0.025 0.052 1.1 0.79 0.61
Source p53.127.F1 p53.127.F1 p53.152.F1 p53 p53
SEQ ID NO: 1312 1313 1314 1315 1316 1317
Sequence FPALNKMF FPALNKMFCQL FPGTRVRAI FPGSTKRAL FPQPKKKPI FPQPKKKPI
\$ ∞
Peptide 48.0055 48.0234 48.0123 48.0127 48.0128

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Table XXIII. Immunogenicity of A2 Supermotif Peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 A*6802 nM nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide ¹	CTL Wild-	CTL
p53.135	6	CQLAKTCPV	1318	208	43.0	143.0	90.06	2	4		1/4	0/4
p53.69	∞	AAPPVAPA	1319	2000	1536	1177	1233	4706	0			
p53.69L2V8	∞	ALPPVAPV	1320	217	7167	200	285	29	• 4	2/4	1/3	0/3
p53.129	6	ALNKMFCQL	1321	735	391	19	73	2	6	i		6
p53.129V9	6	ALNKMFCQV	1322	75	165	7.7	15	i	, 4	0/1		
p53.129B7V9	6	ALNKMFBQV	1323	192	391	23	49	;	- 4	2/2	0/3	<i>C</i> /0
p53.132	6	KMFCQLAKT	1324	333	33	18	106		4		S	710
p53.132V9	6	KMFCQLAKV	1325	33	8.4	7.7	15	ŀ	. 4	1/3	0/2	0/0
p53.132B4V9	6	KMFBQLAKV	1326	125	13	9.1	37	8889	. 4	5/5	0/4 0/4	2/0
p53.132L2V9	6	KLFCQLAKV	1327	86	3.6	3.4	9.5	1270	. 4	2/3	1, 2	t (o
p53.139	6	KTCPVQLWV	1328	725	909	217	15		2			
p53.139L2	6	KLCPVQLWV	1329	122	239	29	23	;	ı 4	2/5	2/3	1/3
p53.139L2B3	6	KLBPVQLWV	1330	45	29	19	31	ł	. 4	3/5	C/2 C/C	1/2
p53.149	6	STPPPGTRV	1331	606	1162	1031	:	129		.	ì	7/1
p53.149L2	6	SLPPPGTRV	1332	122	226	13	9250	140	4	2/3	1/3	۲/0
p53.149M2	6	SMPPPGTRV	1333	172	215	13	425	<i>L</i> 99	4	2/4	2/4	2/2
p53.216	10	VVVPYEPPEV	1334	617	1870	455	1194	;	 - 		j	
p53.216L2	10	VLVPYEPPEV	1335	68	391	71	2056	ľ	· (*)	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1336	1563	1265	2857	507	2999	0		1/1	
p53.255L2V11	11	ILLEDSSGNLV	1337	33	123	71	206	} :	4	1/3	0/3	0/2
												l

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity =10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

				Radiolabeled peptide	l peptide	
	Antigen	Allele	Cell line	Source	Sequence	SEQ ID NO:
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	1338
	A 2	A*0201	УŲ	HBVc 18-27 F6->Y	FLPSDYFPSV	1339
	A 2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV	1340
	A 2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV	1341
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV	1342
	A 2	A*0207	721.221 (transfected	HBVc 18-27 F6->Y	FLPSDYFPSV	1343
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	1344
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	1345
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF	1346
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	1347
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	1348
Ā	A28/68	A*6801	CIR	HBVc 141-151 T7->Y	STLPETYVVRR	1349
₹	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	1350
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTLVYLL	1351
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL	1352
	B27	B*2705	LG2	R 60s	FRYNGLIHR	1353
	B35	B*3501	CIR, BVR	non-natural (B35CON2)	FPFKYAAAF	1354
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	1355
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	1356
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	1357
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	1358
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	1359
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	1360
	Cw4	Cw*0401	CIR	non-natural (C4CON1)	QYDDAVYKL	1361
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	1362
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL	1363
Mouse	D_{p}		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI	1364
	\mathbf{K}_{p}		EL4	VSV NP 52-59	RGYVFQGL	1365
	D^{q}		P815	HIV-IIIB ENV G4->Y	RGPYRAFVTI	1366
	p					1761

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

1368

IPQSLDSYWTSL

HBVs 28-39

P815

 $\Gamma^{\mathbf{q}}$

- -

B. Class II binding assays

en Allele Cell line DRB1*0101 LG2 DRB1*1501 L466.1 DRB1*1601 L242.5 DRB1*1601 L242.5 DRB1*0401 MAT DRB1*0402 YAR DRB1*0404 BIN 40 DRB1*0405 KT3 DRB1*0701 Pitout DRB1*0701 Pitout DRB1*0701 Hill DRB1*1101 Sweig DRB1*1201 Herluf DRB1*1302 H1301 Herluf DRB1*1302 H0301 H257.6 DRB3*0101 MAT DRB3*0101 MAT DRB3*0101 MAT DRB3*0101 MAT DRB3*0101 L257.6 DRB3*0101 MAT DRB3*0101 MAT				•	Radiolal	Radiolabeled peptide	
DR1 DRB1*0101 LG2 DR2 DRB1*1501 L466.1 DR2 DRB1*1601 L242.5 DR3 DRB1*0301 MAT DR4w4 DRB1*0402 YAR DR4w10 DRB1*0402 YAR DR4w14 DRB1*0405 KT3 DR4w15 DRB1*0405 KT3 DR4w15 DRB1*0405 KT3 DR7 DRB1*0405 KT3 DR8 DRB1*0405 KT3 DR9 DRB1*0901 HID DR9 DRB1*0901 HID DR1 DRB1*1101 Sweig DR1 DRB1*1201 Herluf DR1 DRB1*1302 HO301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0101 L255.1 DR53 DRB4*0101 L257.6 DR53 DRB4*0101 L257.6 DR53 DRB4*0101 CH-12 IA* A20 IA* A20 <		Antigen	Allele	Cell line	Source	Sequence	SEQ ID NO:
DR2 DRB1*1501 L466.1 DR3 DRB1*1601 L242.5 DR3 DRB1*0301 MAT DR4w4 DRB1*0402 YAR DR4w16 DRB1*0402 YAR DR4w17 DRB1*0405 YAR DR4w16 DRB1*0405 KT3 DR4w15 DRB1*0405 KT3 DR7 DRB1*0405 KT3 DR7 DRB1*0405 LUY DR9 DRB1*0901 HID DR1 DRB1*0901 HID DR1 DRB1*1101 Sweig DR1 DRB1*1201 Herluf DR1 DRB1*1302 HG301 DR5 DRB1*1302 HG301 DR5 DRB3*0101 GM3107 or L416.3 DR5 DRB3*0101 MAT DR5 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* A20 IR* A20 IR* A20<	Human	DR1	DRB1*0101	TG2	HA Y307-319	YPKYVKQNTLKLAT	1369
DR2 DRB1*1601 L242.5 DR3 DRB1*0301 MAT DR4w4 DRB1*0402 YAR DR4w16 DRB1*0404 BIN 40 DR4w15 DRB1*0405 KT3 DR4w15 DRB1*0405 KT3 DR7 DRB1*0701 Pitout DR8 DRB1*0802 OLL DR9 DRB1*0803 LUY DR9 DRB1*0901 HID DR11 DRB1*1101 Sweig DR13 DRB1*1201 Herluf DR13 DRB1*1302 H0301 DR51 DRB1*1302 HA301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0101 MAT DR51 DRB3*0101 MAT DR51 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* A20 IB* A20 IR* A20 IR* A20		DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY	1370
DR3 DRB1*0301 MAT DR4w4 DRB1*0401 Preiss DR4w10 DRB1*0402 YAR DR4w14 DRB1*0405 YAR DR4w15 DRB1*0405 KT3 DR4w15 DRB1*0701 Pitout DR8 DRB1*0701 Pitout DR9 DRB1*0802 LUY DR9 DRB1*1101 Sweig DR13 DRB1*1101 Sweig DR13 DRB1*1201 Herluf DR51 DRB1*1302 H0301 DR51 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0101 MAT DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* A20 IA* A20 IA* A20 IA* A20 IB* A20 IF* </td <td></td> <td>DR2</td> <td>DRB1*1601</td> <td>L242.5</td> <td>non-natural (760.16)</td> <td>YAAFAAAKTAAAFA</td> <td>1371</td>		DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAAAFA	1371
DR4w4 DRB1*0401 Presiss DR4w10 DRB1*0402 YAR DR4w14 DRB1*0404 BIN 40 DR4w15 DRB1*0405 KT3 DR4w16 DRB1*0405 KT3 DR7 DRB1*0802 OLL DR8 DRB1*0803 LUY DR9 DRB1*1001 Sweig DR11 DRB1*1101 Sweig DR12 DRB1*1201 Herluf DR51 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* A20 IA* A20 IA* A20 IA* A20 IB* A20 IF* A20 IF* A20 IF* A20		DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR	1372
DR4w10 DRB1*0402 YAR DR4w14 DRB1*0404 BIN 40 DR4w15 DRB1*0405 KT3 DR3 DRB1*0701 Pitout DR8 DRB1*0802 OLL DR8 DRB1*0803 LUY DR9 DRB1*0901 HID DR1 DRB1*1101 Sweig DR11 DRB1*1201 Herluf DR12 DRB1*1302 H0301 DR51 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR52 DRB3*0101 MAT DQ3.1 DQ1*041*0301/DQB1*030 PF IA* A20 IA* A20 IA* A20 IA* A20 IA* A20 IB* A20 IF* A20 IF* A20	1	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	1373
DR4w14 DRB1*0404 BIN 40 DR4w15 DRB1*0405 KT3 DR7 DRB1*0701 Pitout DR8 DRB1*0802 OLL DR8 DRB1*0803 LUY DR9 DRB1*0901 HID DR1 DRB1*1101 Sweig DR11 DRB1*1101 Sweig DR12 DRB1*1201 Herluf DR13 DRB1*1201 Herluf DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0101 MAT DR52 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* A20 IA* A20 IA* A20 IA* A20 IF* A20 IF* A20 IF* A20 IF* A20)R4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	1374
DR4w15 DRB1*0405 KT3 DR8 DRB1*0701 Pitout DR8 DRB1*0802 OLL DR9 DRB1*0901 HID DR9 DRB1*1101 Sweig DR11 DRB1*1201 Herluf DR12 DRB1*1201 Herluf DR13 DRB1*1302 Ho301 DR51 DRB5*0101 GM3107 or L416.3 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* A20 IA* A20 IA* A20 IA* A20 IF* A20 IF* A20)R4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	1375
DR7 DRB1*0701 Pitout DR8 DRB1*0802 OLL DR9 DRB1*0901 HID DR11 DRB1*1101 Sweig DR12 DRB1*1201 Herluf DR13 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* A20 IA* A20 IA* A20 IA* A20 IB* A20 IF* A20)R4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	1376
DR8 DRB1*0802 OLL DR8 DRB1*0803 LUY DR9 DRB1*1001 Sweig DR12 DRB1*1201 Herluf DR13 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IB* A20 IF* A20		DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE	1377
DR8 DRB1*0803 LUY DR9 DRB1*0901 HID DR11 DRB1*1101 Sweig DR12 DRB1*1201 Herluf DR13 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20		DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE	1378
DR9 DRB1*0901 HID DR11 DRB1*1101 Sweig DR12 DRB1*1201 Herluf DR13 DRB1*1302 Horluf DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* IA* A20 IA* IA* A20 IA* IB* A20 IA* IF* A20 A20 IF* A20 A20		DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE	1379
DR11 DRB1*1101 Sweig DR12 DRB1*1201 Herluf DR13 DRB1*1302 H0301 DR51 DRB5*0101 CM3107 or L416.3 DR52 DRB3*0101 MAT DR53 DRB4*0101 L255.1 DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA* A20 IA* CH-12 IA* CH-12 IA* A20 IB* A20 IF* A20 IF* A20		DR9	DRB1*0901	CIH	Tet. tox. 830-843	QYIKANSKFIGITE	1380
DR12 DRB1*1201 Herluf DR13 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA ^b DB27.4 IA ^c A20 IA ^c CH-12 IA ^c CH-12 IA ^c A20 IE ^d A20 IF ^c A20 IF ^c A20		DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE	1381
DR13 DRB1*1302 H0301 DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IA ^b DB27.4 IA ^c A20 IA ^c CH-12 IA ^c CH-12 IA ^c A20 IR ^c A20 IF ^c A20 IF ^c A20 IF ^c A20		DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS	1382
DR51 DRB5*0101 GM3107 or L416.3 DR51 DRB3*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 JQA1*0301/DQB1*030 PF IAb DB27.4 IAb A20 IAb A20 IAb A20 IAb A20 IAb A20 IAb A20 IBb A20 IF* A20		DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE	1383
DR51 DRB5*0201 L255.1 DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1 DQA1*0301/DQB1*030 PF IA ^b DB27.4 IA ^k A20 IA ^k CH-12 IA ^b P3.7 IA ^c A20 IF ^k A20 IF ^k A20		DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE	1384
DR52 DRB3*0101 MAT DR53 DRB4*0101 L257.6 DQ3.1)QA1*0301/DQB1*030 PF IAb DB27.4 IA ^k A20 IA ^k CH-12 IA ^k CH-12 IA ^k A20 IF ^k A20		DR51	DRB5*0201	L255.1	HA 307-319	PKYVKQNTLKLAT	1385
DR53 DRB4*0101 L257.6 DQ3.1)QA1*0301/DQB1*030 PF IA ^b DB27.4 IA ^k A20 IA ^k A20 IA ^k CH-12 IA ^k CH-12 IE ^d A20 IE ^d A20		DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL	1386
DQ3.1)QA1*0301/DQB1*030 PF IA ^b DB27.4 IA ^c A20 IA ^c CH-12 IA ^c LS102.9 IA ^c 91.7 IE ^c A20 IF ^k CH-12		DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT	1387
IAb DB27.4 IAb A20 IAb CH-12 IAb LS102.9 IAb 91.7 IEb A20 IFb CH-12			QA1*0301/DQB1*0		non-natural (ROIV)	ҮАНААНААНААНААНАА	1388
A20 CH-12 LS102.9 91.7 A20	Mouse	IAb		DB27.4	non-natural (ROIV)	ҮАНААНААНААНААНАА	1389
CH-12 LS102.9 91.7 A20		IA^d		A20	non-natural (ROIV)	ҮАНААНААНААНААНАА	1390
LS102.9 91.7 A20		IA^k		CH-12	HEL 46-61	YNTDGSTDYGILQINSR	1391
91.7 A20		IAs		LS102.9	non-natural (ROIV)	ҮАНААНААНААНААНАА	1392
A20		IAu		91.7	non-natural (ROIV)	ҮАНААНААНААНААНАА	1393
CH-17		\mathbb{E}^{d}		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK	1394
21-15		IEk		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK	1395

Table XXVI. Crossbinding of A2 supermotif peptides

Source AA	AA	Sequence	SEQ ID NO:	SEQ A*0201 D NO: nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
p53.24	6	KLLPENNVL	1396	313	1955	;	1194		
p53.25	11	LLPENNVLSPL	1397	19	6.2	4.5	12	1702	4
p53.65	10	RMPEAAPPVA	1398	78	102	13	841	1	· (1)
p53.65	6	RMPEAAPPV	1399	119	23	22	70	ł	4
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625	ľ	m
p53.132	6	KMFCQLAKT	1401	333	33	18	106	;	4
p53.135	6	CQLAKTCPV	1402	208	43	143	06	1	4
p53.136	∞	QLAKTCPV	1403	455	ł	100	2643	1067	2
p53.164	6	KQSQHMTEV	1404	200	130	170	285	ł	1 4
p53.187	11	GLAPPQHLIRV	1405	79	39	11	55	;	. 4
p53.193	11	HLIRVEGNLRV	1406	385	1387	83	1194	1778	. 2
p53.229	6	CTTIHYNYM	1407	278	287	2564	561	181	· 60
p53.263	10	NLLGRNSFEV	1408	217	ŀ	2500	881	ł	
p53.264	6	LLGRNSFEV	1409	85	358	37	206	1	4

⁻⁻ indicates binding affinity =10,000nM.

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	Sequence	SEQ ID NO:	A*0201 nM	A*0201 A*0202 A*020 nM nM nM	A*0203 nM	03 A*0206 A*6802 nM nM	A*6802 nM	No. A2 CTL Alleles Wild Crossbound type	CTL Wild- type ¹	CTL
p53.135	135 CQLAKTCPV 1410	1410	208	43	143	06	- 5	4	1/4	0/1

1) Number of donors yielding a positive response/total tested. 2) -- indicates binding affinity =10,000nM.

Table XXVIII. Crossbinding of A2 supermotif analogs

				i															ı						ı		6					
No. A2	Aneles Crossbound	0	4	0	4	3	4	4	1	3	4	4	4	4	4	В	4	4	2	4	4	1	4	4	4	4	1	3	2	4	0	4
A*6802	пМ	4706	29	615	•	1	1	+	;	9 9	. 1	:	8889	1270	:	;	1		:	ł	;	129	<i>L</i> 99	140	ļ		1	:	5333	1569	<i>L</i> 999	;
A*0206	nM	1233	285	514	116	73	15	49	4625	7400	106	15	37	10	06	370	<i>L</i> 9	64	15	23	31	1	425	9250	285	46	1194	2056	974	18	507	206
A*0203	nM	1177	200	1	24	19	7.7	23	71	71	18	7.7	9.1	3.4	143	. 29	15	7.7	217	56	19	1031	13	13	170	35	455	71	<i>L</i> 9	3.6	2857	71
A*0202	nM	1536	7167	968	48	391	165	391	1075	287	33	8.4	13	3.6	43	909	71	119	909	239	29	1162	215	226	130	94	1870	391	391	13	1265	123
A*0201	Мп	2000	217	1786	81	735	75	192	1316	217	333	33	125	86	208	125	102	46	725	122	46	606	172	122	200	122	617	89	<i>L</i> 99	22	1563	33
SEQ ID	NO:	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441
	Sednence	AAPPVAPA	ALPPVAPV	KTYQGSYGFRL	KLYQGSYGFRV	ALNKMFCQL	ALNKMFCQV	ALNKMFBQV	ALNKMFCQLA	ALNKMFCQLV	KMFCQLAKT	. KMFCQLAKV	KMFBQLAKV	KLFCQLAKV	CQLAKTCPV	CLLAKTCPV	BQLAKTBPV	BLLAKTBPV	KTCPVQLWV	KLCPVQLWV	KLBPVQLWV	STPPPGTRV	SMPPPGTRV	SLPPPGTRV	KQSQHMTEV	KLSQHMTEV	VVVPYEPPEV	VLVPYEPPEV	YMCNSSCMGGM	YLCNSSCMGGV	ITLEDSSGNLL	ILLEDSSGNLV
*	AA	∞	8	11	11	6	6	6	10	10	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	6	10	10	11	11	11	
Š	Source	p53.69	p53.69L2V8	p53.101	p53.101L2V1	p53.129	p53.129V9	p53.129B7V9	p53.129	p53.129V10	p53.132	p53.132V9	p53.132B4V9	p53.132L2V9	p53.135	p53.135L2	p53.135B1B7	p53.135B1L2I	p53.139	p53.139L2	p53.139L2B3	p53.149	p53.149M2	p53.149L2	p53.164	p53.164L2	p53.216	p53.216L2	p53.236	p53.236L2M1	p53.255	p53.255L2V1

⁻⁻ indicates binding affinity =10,000nM.

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	¥¥	Sequence	SEQ ID	SEQ ID A*0201	A*0202	A*0203	A*0206 A*6802	A*6802	No. A2	CTL	CTL	CTL
			NO:	пМ	Mu	nM	Mu	nM	Crossbound	Peptide ¹	wild- type	Tumor
p53.69	∞	AAPPVAPA	1442	2000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1443	217	7167	200	285	<i>L</i> 9	4	2/4	1/3	0/3
p53.129	6	ALNKMFCQL	1444	735	391	61	73	2	3			
p53.129V9	6	ALNKMFCQV	1445	75	165	7.7	15	i	4	0/1		
p53.129B7V9	6	ALNKMFBQV	1446	192	391	23	49	i	4	2/4	0/3	0/2
p53.132	6	KMFCQLAKT	1447	333	33	18	106	1	4			
p53.132V9	6	KMFCQLAKV	1448	33	8.4	7.7	15	;	4	1/3	0/2	0/2
p53.132B4V9	6	KMFBQLAKV	1449	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	6	KLFCQLAKV	1450	86	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	6	KTCPVQLWV	1451	725	909	217	15	;	2			
p53.139L2	6	KLCPVQLWV	1452	122	239	59	23	;	4	2/5	2/3	1/3
p53.139L2B3	6	KLBPVQLWV	1453	45	29	19	31	;	4	3/4	2/3	1/2
p53.149	6	STPPPGTRV	1454	606	1162	1031	;	129		-		
p53.149L2	6	SLPPPGTRV	1455	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	6	SMPPPGTRV	1456	172	215	13	425	<i>L</i> 99	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1457	617	1870	455	1194	:	-			
p53.216L2	10	VLVPYEPPEV	1458	68	391	71	2056	ł	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1459	1563	1265	2857	507	2999	0			
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	ł	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested. 2) -- indicates binding affinity =10,000nM.

Table XXX. DR supertype primary binding

	Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
	39.0307	2	GFRLGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
	39.0308	2	LNKMFCQLAKTCPVC	1462	P53.130	20	804	167	3
	39.0309	2	MGGMNRRPILTITL	1463	P53.243				0
٠	39.0309	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500		0
	39.0310	2	KRALPNNTSSSPQPK	1465	P53.305				0
	39.0311	2	DGEYFTLQIRGRERF	1466	P53.324	125			1

⁻⁻ indicates binding affinity =10,000nM.

Table XXXI. DR supertype cross-binding

:		SEQ ID		DR1	DR4w4	DR7	DR2w2	DR2w2	DR6w1	DR2w2 DR2w2 DR6w1 DR5w1 DR8w2 DR147	DR8w2		Broad
Peptide	Sequence	NO:	Source	Mu	Mu	Ми	β1 nM	β1 nM β2 nM 9 nM	Mu 6	l nM	nM	nM Binding	(5/8)
39.0307	GFRLGFLHSGTAKSV	1467	p53.108 2.6	2.6	5.4	68	253	167	9/	100	56	3	8
39.0308	39.0308 LNKMFCQLAKTCPV	1468	p53.130	20	804	167	2688	541	365	2500	1531	3	5

-- indicates binding affinity = 10,000nM.

All Down

Table XXXII. DR3 binding

Peptide	Sequence	SEQ ID NC	Source	DR3 nM
39.0409	EPPLSQETFSDLWKL	1469	p53.11	
39.0410	LWKLLPENNVLSPLP	1470	p53.22	
39.0411	DLMLSPDDIEQWFTE	1471	p53.42	
39.0412	EQWFTEDPGPDEAPR	1472	p53.51	
39.0413	PVQLWVDSTPPPGTR	1473	p53.142	
39.0414	MAIYKQSQHMTEVVR	1474	p53.160	
39.0415	QHLIRVEGNLRVEYL	1475	p53.192	3125
39.0416	LIRVEGNLRVEYLDD	1476	p53.194	3226
39.0417	EGNLRVEYLDDRNTF	1477	p53.198	
39.0418	RVEYLDDRNTFRHSV	1478	p53.202	1667
39.0419	SVVVPYEPPEVGSDC	1479	p53.215	
39.0420	PPEVGSDCTTIHYNY	1480	p53.222	7895
39.0421	LTIITLEDSSGNLLG	1481	p53.252	
39.0422	KKPLDGEYFTLQIRG	1482	p53.320	
39.0423	GEYFTLQIRGRERFE	1483	p53.325	
39.0424	RFEMFRELNEALELK	1484	p53.337	

⁻⁻ indicates binding affinity =10,000nM.

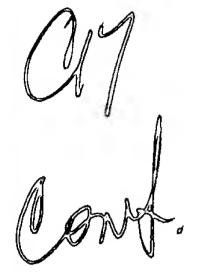


Table XXXIII. HTL candidate peptides

0
8
m m
29 1531
100 2500
76 365
167 541
253 5688
1 1
89
5.4
2.6
HSGTAKSV 1485p53.108
39.0307 GFRLGFLHSGTAKSV 1485p53.108 39.0308 LNKMFCQLAKTCPVQ 1486p53.130
<u>r</u> ∞

-- indicates binding affinity = 10,000nM.

					Colon
Table IV.	HLA Class I Sta	andard Peptide Bindin	ng	Affinity.	
ALLELE	STANDARD	SEQUENCE		SEQ ID NO:	STANDARD
	PEPTIDE				BINDING AFFINITY
					(nM)
A*0101	944.02	YLEPAIAKY		1189	25
A*0201	941.01	FLPSDYFPSV		1190	½5.0
A*0202	941.01	FLPSDYFPSV		1191	4.3
A*0203	941.01	FLPSDYFPSV	1	1192	10
A*0205	941.01	FLPSDYFPSV	1	1193	4.3
A*0206	941.01	FLPSDYFPSV	Ì	1194	3.7
A*0207	941.01	FLPSDYFPSV		1195	23
A*6802	1072.34	YVIKVSARV		1196	8.0
A*0301	941.12	KVFPYALINK		1197	11
A*1101	940.06	AVDLYHFLK		1198	6.0
A*3101	941.12	KVFPYALINK		1199	18
A*3301	1083.02	STLPETYVVRR	1	1200	29
A*6801	941.12	KVFPYALINK	1	1201	8.0
A*2402	979.02	AYIDNYNKF	1	1202	12
B*0702	1075.23	APRTLVYLL		1203	5.5
B*3501	1021.05	FPFKYAAAF	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	1204	7.2
B51	1021.05	FPFKYAAAF	ľ	1205	5.5
B*5301	1021.05	FPFKYAAAF		1206	9.3
B*5401	1021.05	FPFKYAAAF	1	1207	10
	ı .				

Table V. HLA Class II Standard Peptide Binding Affinity.

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Allele	Nomenclature	Standard	Sequence	SEQ	Binding
		Peptide		ID	Affinity
				NO:	(nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2β1	507.02	GRTQDENPVVHFFKNIVTP	1220	9.1
			RTPPP		
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT		58
DRB5*0101	DR2w2β2	553.01	QYIKANSKFIGITE		20
				1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

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VIONO NO		DR5w11 DR5w12						0.2000			0.0080										
	• •	DR4w15																			
HOM		ding Data DR4w4			-0.0027			8.3000		-0.0027	0.0560	-0.0027					0.0100				
		Super Motif Peptides with Binding Data DR2w81 DR2w2B2 DR3 DR4w				0.0150	0.0039	0.0027			0.0006	0.0030		0.0380					-0.0025		
) () ()	S .	tif Peptides 1 DR2w2B2						0.1200			0.0370										
) >	Super Mot DR2w81						0.0360			0.0016										
		p53 DR			0.0400			1.9000		-0.0005	0.2500	-0.0005				0.0010					
		XIX 117 Position 118	119	\$ 88 8	324	7 ~ £	13.8	50 27 50 27	234 4 233 4 5 233 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	305	32	252 243 169	345 29 29	222 142 144	110	209 249 248	269 261	37 (8	21S 80 S	203	217 23 234
- - رند	•	Table XIX Exemplary SeqID Num	1058	1060	1063	1065			1072	1075	1078	1080	1083	1086	1089	1092 1093	1094	1097	9011	1102	1105
30		Exemplary Sequence	SVTCTYSPALNKM ELKDAQAGKEPGG PVAPAPAAPTPAA	RMPEAAPPVAPAP SWPLSSSVPSQKT	CI IIHYNYMCNSSCM DGEYFTLQIRGRERF DLMLSPDDIEOWFTE	DPSVEPPLSQETFSD EGNLRVEYLDDRNTF	ENNVLSPLPSQAMDD FCQLAKTCPVQLWVD FSDI WKI I PENNYI S	GFRLGFLHSGTAKSV GTRVRAMAIYKQSQH	HHELPFGSTKRALPN HSVVVPYEPPEVGSD HYNYMCNSSCMGGMN	IEQWFTEDPGPDEAP KRALPNNTSSSPQPK LGFLHSGTAKSVTCT	LNKMFCQLAKTCPVQ LSPLPSQAMDDLMLS	LTIITLEDSSGNLLG MGGMNRRPILTIITL MTEVVRRCPHHERCS	NEALELKDAQAGKEP NNVLSPLPSQAMDDL PDDIEQWFTEDPGPD	PPEVGSDCTTIHYNY PVQLWVDSTPPPGTR QLWVDSTPPPGTRVR	RLGFLHSGTAKSVTC RNSFEVRVCACPGRD	KNIFKHSVVVPYEPP RPILTITLEDSSGN RRPILTITLEDSSG	SFEVRVCACPGRDRR SGNLLGRNSFEVRVC SPAI NKMECOLAVIC	SQAMDDLMLSPDDIE SSSVPSQKTYQGSYG	SWPLSSSVPSQKTYQ SYGFRLGFLHSGTAK	VEYLDDRNTFRHSVV VQLWVDSTPPPGTRV	TEPFEVGSDCTT LPENNVLSPLPS MCNSSCMGGMNR
9		Core SeqID Num	* 4 4								٠-٠٠ ـ.		_			R R R	SFEVRV SGNLLG SPAINK	SQAMDE	SWPLSS: SYGFRL	VEYLDD VQLWVI	WKLLPE YNYMCN
				==:			1134			1141 1142 1143	==	1146 1147 1148	1149	===	==:	=======================================	1160	28.2	1166	1168	1171
		Core	VTCTYSPAL LKDAQAGKE VAPAPAAPT	MPEAAPPVA WPLSSSVPS	YFTLQIRGR LSPDDIEQW	VEPPLSQET LRVEYLDDR	VLSPLPSQA LAKTCPVQL LWKLLPENN	LGFLHSGTA VRAMAIYKQ	VVPYEPPEV YMCNSSCMG	WFIEDPGFD LPNNTSSSP LHSGTAKSV	MFCQLAKTC LPSQAMDDL	MNRRPILTI VVRRCPHHE	LELKDAQAG LSPLPSQAM IEQWFTEDP	VGSDCTTIH LWVDSTPPP VDSTPPPGT	FLHSGTAKS FEVRVCACP FRHSVVVVDV	LTITLEDS	VKVCACFGK LLGRNSFEV LNKMFCOLA	MDDLMLSPD VPSQKTYQG VPYFPPFVG	LSSSVPSQK FRLGFLHSG	LDDRNTFRH WVDSTPPPG VFPPFVGSD	LPENNVLSP MCNSSCMGG

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r		DRw53																									
	200	ata DR9																									
3	9,	n Binding D DR8w2							1.7000				0.0320														
0 1	Ø)	Peptides with Binding Data DR7 DR8w2			81000	0.0010			0.2800			-0.0007	0.1500		-0.0007						0.0023						
O Jan		Super Motif P DR6w19							0.0460				9600.0													,	
		Exemplary SeqID Num	1057 1058	1059	1062	1064	9901	1068	1070	1072	1074	1075 1076	1077	1079	1081	1083	1085	1087	6801	1091	1093	1095	1097	1099	101	1103	1105
		Exemplary Exe Sequence Seq	SPALNKM	AAPTPAA	PSWPLSSSVPSQKT	IKGKEKF	LDDRNTF	PVQLWVD PVQLWVD	SGTAKSV	TKRALPN	HYNYMCNSSCMGGMN	PGPDEAP FSSSPQPK	LGFLHSGTAKSVTCT LNKMFCQLAKTCPVQ	SPLPSQAMDDLMLS	MGGMNRRPILTIITL	NEALELKDAQAGKEP	PDDIEQWFTEDPGPD	PVQLWVDSTPPPGTR	ALGFLHSGTAKSVTC	RNTFRHSVVVPYEPP	RPILTIITLEDSSGI RRPILTIITLEDSSG SEEVRVCA CPGRDRR	SGNLLGRNSFEVRVC	SQAMDDLMLSPDDIE	SVVVPYEPPEVGSDC	SYGFRLGFLHSGTAK STORY	VELLUDINALITADISTY VQLWVDSTPPPGTRV VVPVFPPFVGSDCTT	WKLLPENNVLSPLPS YNYMCNSSCMGGMNR
OD O		Tab Exen Seq	AKSVTCTYSPALNKM AI FI KDAOAGKEPGG	APPVAPAPAAPTPAA APRMPEAAPPVAPAP	APSWPLSSSVPSQKT CTTIHYNYMCNSSCN	DCEYFILQIRGREKE DLMLSPDDIEQWFTE	DPSVEPPLSQEIFSD EGNLRVEYLDDRNTF	FCQLAKTCPVQLWVD	GFRLGFLHSGTAKSV	GI KVKAMAI Y KUSUH HHELPPGSTKRALPN	HSVVVPYEPPEVGSD HYNYMCNSSCMGGN	IEQWFTEDPGPDEAP KRALPNNTSSSPQPK	LGFLHSGT LNKMFCQI	LSPLPSQAMDDLM 1 TITT EDSSGNLLG	MGGMNRRPILTITL MTEXXVB RCPHHER	NEALELKE NEALELKE	PDDIEQWFTEDPGPD PBEVGSDCTTHXNV	PVQLWVD	RLGFLHSC	RNTFRHS	RRPIL TIITLEDSSGIN RRPIL TIITLEDSSG	SGNLLGR	SQAMDDL	SVVVPYEI STAND	SYGFRLGI SYGFRLGI	VEILUUR VQLWVDS VVPVFPPI	WKLLPEN
		Core SeqID	1123	1125	1127	1130	1132	1134	1136	1138	1139	1141 1142	1143	1145	1147	1149	1151	1153	1155	1157	1159	1911	1163	1165	1167	1169	1171
			, 4		~ ×	- 1 >	. &	: د ر	Z ~	O		Ω.	> C	. H.	[# U 2	الاما:	T & 1	- S ;	2 , ≽	Ę		5 Q S	<u>ე</u> . ლ. ;	∡ დ	5 Ç c	G P C
		Core	VTCTYSPAL	VAPAPAAPT MPEAAPPVA	WPLSSSVPS IHYNYMCNS	YFTLQIRGR LSPDDIEQW	VEPPLSQET LRVEYLDDR	VLSPLPSQA LAKTCPVQL	LWKLLPENN LGFLHSGTA	VRAMAIYKQ LPPGSTKRA	VVPYEPPEV YMCNSSCMG	WFTEDPGPD	LHSGTAKSV MFCOLAKTC	LPSQAMDDL	MNRRPILTI	VVKKCPHHE LELKDAQAG	LSPLPSQAM IEQWFTEDP	LWVDSTPPP	FLHSGTAKS	FEVRVCACE	LTHTLEDS LTHTLED	LLGRNSFEV	MDDLMLSPD	VPYEPPEVG	FRLGFLHSG	WVDSTPPPG	LPENNVLSP MCNSSCMGO

	DR5w12														
	DR5w11														
ָ ב ב	ng Data DR4w15														
Control of the Control of the Product Date	DR4w4														
Motif Pontin	DR3	0.0150	0.0039	-0.0025	-0.0025	-0.0025	0.0030	0.0029	0.0380	0.0300	0.0960	0.0052	0.1800	-0.0025	
	2w2B1														
Toble XX.	DRI DR														
	Position	42	198		51	320	∦ 252	22	222	142	192	337	202	215	
	Exemplary Position SeqID Num.	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	6111/	
	Exemplary Sequence	DLMLSPDDIEQWFTE	EGNLRVEYLDDRNTF	EPPLSQETFSDLWKL	EQWFTEDPGPDEAPR	KKPLDGEYFTLQIRG	LTITLEDSSGNLLG	LWKLLPENNVLSPLP	PPEVGSDCTTIHYNY	PVQLWVDSTPPPGTR	OHLIRVEGNLRVEYL	RFEMFRELNEALELK	RVEYLDDRNTFRHSV	SVVVPYEPPEVGSDC	
	Core SeqID	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	
	Core	LSPDDIEQW	LRVEYLDDR	LSQETFSDL	FTEDPGPDE	LDGEYFTLQ	ITLEDSSGN	LLPENNVLS	VGSDCTTIH	LWVDSTPPP	IRVEGNLRV	MFRELNEAL	YLDDRNTFR	VPYEPPEVG	

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	DRw53	
	DR9	
Motif Peptides with Binding Data	DR8w2	
ides with B	DR7	
Motif Pept	DR6w19	
p53_DR-3a	Exemplary SeqID Num	1107 1108 1109 1111 11115 11118 11118 11118
Table XXa	Exemplary Sequence	DLMLSPDDIEQWFTE EGNLRVEYLDDRNTF EPPLSQETFSDLWKL EQWFTEDPGPDEAPR KKPLDGEYFTLQIRG LTIITLEDSSGNLLG LWKLLPENNVLSPLP PPEVGSDCTTIHYNY PVQLWVDSTPPPGTR QHLIRVEGNLRVEYL RFEMFRELNEALELK RVEYLDDRNTFRHSV SVVVPYEPPEVGSDC
A.	Core SeqID Num	1173 1174 1175 1176 1177 1179 1180 1181 1181 1183
•	Core	LSPDDIEOW LRVEYLDDR LSOETFSDL FTEDPGPDE LDGEYFTLO ITLEDSSGN LLPENNVLS VGSDCTTIH LWVDSTPPP IRVEGNLRV MFRELNEAL YLDDRNTFR VPYEPPEVG

DR5w12	
ing Data DR4w15 DR5w11	1. th
s with Bind DR4w4	
tif Peptide: DR3	0.0290 0.0930 -0.0025
p53 DR 3b Motif Peptides with Binding Data	
Table XXb	
Position	325 194 160
Exemplary SeqID Num	1120
Core SeqID Exemplary Sequence	1186 GEYFTLQIRGRERFE 1187 LIRVEGNLRVEYLDD MAIYKQSQHMTEVVR
	FTLQIRGRE VEGNLRVEY YKQSQHMTE

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inding Data DRw53					•	`	
s with B			1	<i></i>			
p53 DR 3b Motif Peptides with Binding Data DR7 DR8w2 DR9 DRw53			4 17.				
p53 DR 3				::" "J			<u></u> .
able XXb	SeqID Num	1120					
	Sequence Core Seq1D Exemplary Sequence Num Sequence Seq1E	RE 1186 GEYFTLQIRGRERFE VEY 1187 LIRVEGNLRVEYLDD MTE 1188 MAIYKQSQHMTEVVR			•		

9		136			, w
Table XXII.	A2 si	upermotif anal	ogs		7.50 M
			11		
		_	SEQ	A*0201	
Source	AA	Sequence	ID	nM	
			NO:		
p53.24	9	KLLPENNVL	1224	313	
p53.24V9	9	KLLPENNVV	1225	385	
p53.25	11	LLPENNVLSPL	1226	19	
p53.25V9	11	LLPENNVLSPV	1227	39	
p53.65	9	RMPEAAPPV	1228	119	
p53.65L2	9	RLPEAAPPV	1229	78 70	
p53.65	10	RMPEAAPPVA	1230	78	
p53.65L2V10	10	RLPEAAPPVV	1231	143	
p53.65M2V10	10	RMPEAAPPVV	1232	54	
p53.69	8	AAPPVAPA	1233	5000	
p53.69L2V8	8	ALPPVAPV	1234	217	
p53.101	11	KTYQGSYGFRL	I .	1786	
p53.101L2V11		KLYQGSYGFRV	1236	81	
p53.113	11	FLHSGTAKSVT	1237	5000	
p53.113V11		FLHSGTAKSVV	1238	1220	
p53.129	9	ALNKMFCQL	1239	735	
p53.129V9	9	ALNKMFCQV	1240	75	
p53.129B7V9	9	ALNKMFBQV	1241	192	
p53.129	10	ALNKMFCQLA	1242	1316	
p53.129V10	10	ALNKMFCQLV	1243	217	
p53.132	9	KMFCQLAKT	1244	333	
p53.132V9	9	KMFCQLAKV	1245	33	
p53.132B4V9	9	KMFBQLAKV	1246	125	
p53.132L2V9	9	KLFCQLAKV	1247	98	
p53.135	9	CQLAKTCPV	1248	208	
p53.135L2	9	CLLAKTCPV	1249	125	
p53.135B1B7	9	BQLAKTBPV	1250	102	
p53.135B1L2B7	9	BLLAKTBPV	. 1251	46	
p53.139	9	KTCPVQLWV	1252	725	
p53.139L2	9	KLCPVQLWV	1253	122	
p53.139L2B3	9	KLBPVQLWV	1254	46	
p53.149	9	STPPPGTRV	1255	909	
p53.149M2	9	SMPPPGTRV	1256	172	
p53.149L2	9	SLPPPGTRV	1257	122	
p53.164	9	KQSQHMTEV		500	
p53.164L2	9	KLSQHMTEV		122	
p53.216	10	VVVPYEPPEV	1260	617	
p53.216L2	10	VLVPYEPPEV	1261	89	
p53.229	9	CTTIHYNYM	1262	278	
p53.229L2V9	9	CLTIHYNYV	1263	263	
p53.229B1L2V9		BLTIHYNYV		116	
p53.236	8	YMCNSSCM	1265	4546	
p53.236L2M8	8	YLCNSSCV	1266		
p53.236	11	YMCNSSCMGGM		667	
p53.236L2M11		YLCNSSCMGGV		22	
p53.255	11	ITLEDSSGNLL		1563	
p53.255L2V11		ILLEDSSGNLV		33	
p53.256	10	TLEDSSGNLL	1271	1667	_
p53.256V10	10	TLEDSSGNLV	1272	4167	-

Table XXIIA A01 Analog Peptides

Peptide 52.0136 57.0035 57.0125 57.0126 57.0127	<u>AA</u> 11 9 10 10	Sequence GSDCTTIHYNY GTDCTTIHY PTQKTYQGSY GTDKSVTCTY RVDGNLRVEY	SEQ II 12 12 12 12 12 127	73 p53.226 74 p53.226.T2 75 p53.98.T2 76 p53.117.D3	A*0101 nM 67.6 0.9 35.7 42.4 45.5
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KVYQGSYGFK	BVYSPALNK	BVYSPALNR	KVFBQLAK	GVRVRAMAIYK	RVRAMAIYR	SVBMGGMNK	SVBMGGMNRK	SVBMGGMNR	SVBMGGMNRR	RVBABPGRDRK	SVSRHKKLMFK	SVSRHKKLMFR
9	6	თ	ω	7	თ	တ	10	6	10	7	7	-
1371.15	1371.16	1371.17	1371.18	1371.2	1371.22	1371.24	1371.25	1371.26	1371.27	1371.31	1371.32	1371.33
	5 10	5 10 6	ე ე ი ი	<u>ე</u> თ თ დ	2 9 9 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5	Ç o o o t o	Ç o o ∞ , o o	Ç o o ≈ ± o o c	Ç o o ∞ t o o c o	C v v v c v c v c v c v c v c v c v c v	Ç o o o c o c t	\$ 6 6 6 6 5 T T

A3 XRN	4	4	4	Ŋ	_	က	က	က	က	4	2	2	က	ო
A*6801 nM A		38.1	200	14.8	8888.9	13333.3	2.999	29.6	17	11.1	11.4	2500	1509.4	200
A*3301 nM	10000	-72500	22307.7	85.3	-72500	-72500	138.1	-72500	-72500	852.9	805.6	-72500	18125	1381
A*3101 nM	72	138.5	439	33.3	7500	418.6	8.6	0006	-36000	120	620.7	4615.4	295.1	183.7
A*1101 nM	61.9	9.2	12.8	8.3	461.5	136.4	1666.7	17.1	75	95.2	25	200	54.5	2857.1
A*0301 nM	37.9	33.3	15.7	25	846.2	57.9	40.7	12.5	100	161.8	1000	314.3	33.3	196.4
Source	p53.101.V2	p53.101.V2K10	p53.124.B1V2	p53.124.B1V2R9	p53.132.V2B4	p53.154.V2	p53.156.R9	p53,240.V2B3K9	p53.240.V2B3K10	p53.240.V2B3	p53.240.V2B3	p53.273.B3B5K11	p53.376.V2	p53.376.V2R11
SEO ID NO:	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291

Table XXIIC A02 Analog Peptides

A2 XRN 3	თ 4 4 w ← w
A*6802 nM -40000	-80000 -80000 -80000 -80000 80000
A*0206 nM 92.5	72.5 105.7 284.6 560.6 1193.5 4625
A*0203 nM 19.6	18.5 17.5 169.5 2564.1 12500 14.5
	390.9 33.1 130.3 286.7 1954.5 179.2
A*0201 nM 505.1 41.7 27.8	735.3 333.3 500 277.8 312.5 357.1
Source p53 132 mp53.261 mp53.261	p53.129 p53.164 p53.229 p53.24 p53.113
SEQ ID NO: Source 1292 p53 13; 1293 mp53.2 1294 mp53.2	1296 1297 1298 1299 1300
Sequence KMFCQLAKT LLGRDSFEV LLGRDSFEV ALMKMFCOL	KMFCQLAKT KQSQHMTEV CTT!HYNYM KLLPENNVL FLHSGTAKSV
∯ തതത	000000
Peptide 27.0068 39.0074 44.0003	1317.23 1324.08 1329.04 1329.07 1329.09

-added

Table XXIID A24 Analog Peptides

			(-		
Table XXIII	D A24 Aı	nalog Peptides	J.	Para Colo	
Peptide Peptide	AA	Sequence	SEQ ID NO:	Source	A*2401 nM
52.008	<u>AA</u> 8	TYQGSYGF	1301	∥ p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0103	10	TYQGSYGFRL	1303 //	p53.102	100
52.0104	10	TYSPALNKMF	1304 //	p53.125	2.4
52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0147	11	TYLWWVNGQSL	∖ 1306 ∥	CEA.531	92.3
57.0042	9	LYWVNGQSF	\ 1307	CEA.533.Y2F9	15.8
57.0051	9	EYVNARHCF	\\ 1308	Her2/neu.553.F9	150
57.007	9	TYSDLWKLF	∖ 1309 /	p53.18.Y2F9	5.5
57.0071	9	SYGFRLGFF	1310 ∥	p53.106.F9	121.2
57.0096	10	TYQGSYGFRF	1311	p53.102.F10	30

TABLE XXIIE B07 Analog Peptides

Z)
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
8*5401 nM 3846.2 500 2439 -20000 16666.7 -100000
8*5301 nM 6200 7750 23250 -31000 -31000
B*5101 nM 18333.3 5500 662.7 6111.1 -55000
8*3501 nM 3000 2482.8 -36000 -36000 -36000
B*0702 nM 0.025 0.052 1.1 0.79 0.61 2.3
Source p53.127.F1 p53.127.F1 p53.152.F1 p53 p53 p53 p53
SEQ ID NO: 1312 1313 1314 1315 1316 1317
Sequence FPALNKMF FPALNKMFCQL FPGTRVRAI FPQPKKKPI FPQPKKKPL
№ 1 0 0 0 0 .
Peptide 48.0055 48.0234 48.0123 48.0127 48.0128

Table XXIII. Immunogenicity of A2 Supermotif Peptides

				-								1
Source	AA A	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide ¹	CTL Wild-	CTL
								,	CIOSSOCIA			
p53.135	6	COLAKTCPV	1318	208	43.0	143.0	0.06	`	4		1/4	0/4
n53 69	∞	AAPPVAPA	1319	2000	1536	1177	1233	4706	0			,
p53.69L2V8	· ∞	ALPPVAPV	1320	217	7167	200	285	29	4	2/4	1/3	0/3
053.129	6	ALNKMFCQL	1321	735	391	19	73	- 5	3			
p53.129V9	6	ALNKMFCOV	1322	75	165	7.7	15	ŀ	4	0/1		;
p53.129B7V9	6	ALNKMFBQV	1323	192	391	23	49	-	4	2/4	0/3	0/2
p53.132	6	KMFCQLAKT	1324	333	33	18	106	1	4			9
n53 132V9	6	KMFCOLAKV	1325	33	8.4	7.7	15	;	4	1/3	0/5	0/2
53 132B4V9	. 0	KMFBOLAKV	1326	125	13	9.1	37	6888	4	2/2	0/4	0/4
p53.132L2V9	, 6	KLFCOLAKV	1327	86	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
n53 139	6	KTCPVOLWV	1328	725	909	217	15	:	7			·
n53.1391.2	. 6	KLCPVQLWV	1329	122	239	53	23	ł	4	2/5	2/3	1/3
n53.139L2B3	6	KLBPVQLWV	1330	45	29	19	31	:	4	3/4	2/3	1/2
p53.149	6	STPPPGTRV	1331	606	1162	1031	;	129	_			!
p53.149L2	6	SLPPPGTRV	1332	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	6	SMPPPGTRV	1333	172	215	13	425	299	4	2/4	2/4	2/4
053.216	10	VVVPYEPPEV	1334	617	1870	455	1194	:	,		;	
p53.216L2	10	VLVPYEPPEV	1335	68 //	391	71	2056	:	3	1/1	1/1	
053.255	=	ITLEDSSGNLL	1336	1563	1265	2857	207	<i>L</i> 999	0		;	
p53.255L2V11	11	ILLEDSSGNLV	1337	33	123	71	206	:	4	1/3	0/3	0/2
				45								

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity =10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

	SEO ID NO:	1338	1339	1340	1341	1342	1343			1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366)) -
ed peptide	Sequence	YTAVVPLVY	FLPSDYFPSV	FLPSDYFPSV	FLPSDYFPSV	FLPSDYFPSV	FLPSDYFPSV	KVFPYALINK	KVFPYALINK	AYIDNYNKE	KVFPYALINK	KVFPYALINK	STLPETYVVRR	FTQAGYPAL	APRTLVYLL	FLKDYQLL	FRYNGLIHR	FPFKYAAAF	FPFKYAAAF	FPFKYAAAF	AEMGKYSFY	FPFKYAAAF	FPFKYAAAF	FPFKYAAAF	QYDDAVYKL	YRHDGGNVL	YRHDGGNVL	SGPSNTYPEI	RGYVFOGL	RGPYRAFVTI	
Radiolabeled peptide	Source	Hu. J chain 102-110	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	non-natural (A3CON1)	non-natural (A3CON1)	non-natural (A24CON1)	non-natural (A3CON1)	non-natural (A3CON1)	HBVc 141-151 T7->Y	HBV pol 646-654 C4->A	A2 sigal seq. 5-13 (L7->Y)	IVgp 586-593 Y1->F, Q5->	R 60s	non-natural (B35CON2)	non-natural (B35CON2)	non-natural (B35CON2)	EF-1 G6->Y	non-natural (B35CON2)	non-natural (B35CON2)	non-natural (B35CON2)	non-natural (C4CON1)	non-natural (C6CON1)	non-natural (C6CON1)	Adenovirus E1A P7->Y	VSV NP 52-59	HIV-IIIB ENV G4->Y	
•	Cell line	Steinlin	ЛY	P815 (transfected)	FUN	CLA	'21.221 (transfected	GM3107	BVR	KAS116	SPACH	LWAGS	CIR		_	L		C1R, BVR	TISI	EHM	PITOUT	KAS116	AMAI	KT3	CIR	721.221 transfected	721.221 transfected	EL4	EL4	P815	
;	Allele	A*0101	A*0201	A*0202	A*0203	A*0206	A*0207			A*2402	A*3101	A*3301	A*6801	A*6802	B*0702	B*0801	B*2705	B*3501	B*3502	B*3503	B*4403	•	B*5301	B*5401	Cw*040]	Cw*0602	Cw*0702				
	Species Antigen	Human Al	A2	A2	A2	A2	A2	A 3	A11	A24	A31	A33	A28/68	A28/68	B/	P8	B27	B35	B35	B35	B44	B51	B53	B34	CW4	Cwb	(w)	Mouse D ^b	$\mathbf{K}_{\mathbf{p}}$	۵	~

Table XXIV. MHC-peptide binding assays: cell lines and radiolaheled ligands

ı ilgands.	1368
and assubs. Con mics and radiolabeted ligands.	IPQSLDSYWTSL
mems assays.	HBVs 28-39
	P815
p ·	T

assays
binding
B. Class II

	SEO ID NO:	360	370	1371	1372	1373	1374	375	376	377	. 8/	62	30	31	32	3 2	7 .		2 %		&	6	9		5	č.	4	
1	AFO I	13	7 -	7 2		3	7	7	13,	13.	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	
Radiolabeled pentide	Sequence	YPKYVKONTI KI AT	VVHFFKNIVTPRTPPY	YAAFAAAKTAAAFA	YKTIAFDEEARR	YARFOSOTTLKOKT	YARFOROTTLKAAA	YARFOSOTTLKOKT	YARFOSOTTLKOKT	QYIKANSKFIGITE	QYIKANSKFIGITE	QYIKANSKFIGITE	QYIKANSKFIGITE	QYIKANSKFIGITE	EALIHQLKINPYVLS	OYIKANAKFIGITE	OYIKANAKFIGITE	PKYVKONTLKLAT	NGOIGNDPNRDIL	YARFQSQTTLKQKT	ҮАНААНААНААНААНА	ҮАНААНААНААНАА	ҮАНААНААНААНАА	YNTDGSTDYGILQINSR	ҮАНААНААНААНАА	ҮАНААНААНААНАА	YLEDARRKKAIYEKKK	VIEDABBUVARRUUM
Radiol	Source	HA Y307-319	MBP 88-102Y	non-natural (760.16)	MT 65kD Y3-13	non-natural (717.01)	non-natural (717.10)	non-natural (717.01)	non-natural (717.01)	Tet. tox. 830-843	unknown eluted peptide	Tet. tox. 830-843 S->A	Tet. tox. 830-843	HA 307-319	Tet. tox. 830-843	non-natural (717.01)	non-natural (ROIV)	non-natural (ROIV)	non-natural (ROIV)	HEL 46-61	non-natural (ROIV)	non-natural (ROIV)	Lambda repressor 12-26	7 Cl. "Concernor of the I				
	Cell line	LG2	L466.1	L242.5	MAT	Preiss	YAR	BIN 40	KT3	Pitout	OLL	LUY	HID	Sweig	Herluf	H0301	GM3107 or L416.3	L255.1	MAT	Ţ	50 PF	DB27.4	A20	CH-12	LS102.9	91.7	A20	CH-12
	Allele	DRB1*0101	DRB1*1501	DRB1*1601	DRB1*0301	DRB1*0401	DRB1*0402	DRB1*0404	DRB1*0405	DRB1*0701	DRB1*0802	DRB1*0803	DRB1*0901	DRB1*1101	DRB1*1201	DRB1*1302	DRB5*0101	DRB5*0201	DRB3*0101	DRB4*0101	JQA1*U3UI/DQB1*030							
	Species Antigen	Human DR1	DR2	DR2	DR3	DR4w4	DR4w10	DR4w14	DR4w15	DR7	DR8	DR8	DR9	DKII	DRIZ	DR13	DRSI	DR51	DR52		1.6)	Mouse IA ⁵	IAu	IA*	ĬĄ"	ĮΥ.	IE.	ΙΕ̈́

Table XXVI. Crossbinding of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0202 A*0203 A*0206 A*6802 nM nM nM nM	A*6802 nM	No. A2 Alleles Crossbound
p53.24	6	KLLPENNVL	1396	313	1955	;	1194		-
p53.25	11	LLPENNVLSPL	1397	19	6.2	4.5	12	1702	4
p53.65	10	RMPEAAPPVA	1398	78	102	13	841	1	κ
p53.65	6	RMPEAAPPV	1399	119	23	22	70	ł	4
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625	i	. ω
p53.132	6	KMFCQLAKT	1401	333	33	18	106	;	4
p53.135	6	CQLAKTCPV	1402	208	43	143	90	;	. 4
p53.136	∞	QLAKTCPV	1403	455	;	100	2643	1067	. c
p53.164	6	KQSQHMTEV	1404	200	130	170	285	· ;	1 4
p53.187	1	GLAPPQHLIRV	1405	62	39	11	55	;	. 4
p53.193	11	HLIRVEGNLRV	1406	385	1387	83	1194	1778	. 0
p53.229	6	CTTIHYNYM	1407	278	287	2564	561	181	l m
p53.263	10	NLLGRNSFEV	1408	217	ł	2500	881	;	,
p53.264	6	LLGRNSFEV	1409	85	358	37	206	;	4

-- indicates binding affinity =10,000nM.

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	Sequence	SEQ ID NO:	A*0201 nM	4*0201 A*0202 A*0203 A*0206 A*6802 nM nM nM nM nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 CTL Alleles Wild Crossbound type	CTL Wild- type ¹	CTL
p53.135	CQLAKTCPV 1410	1410	208	43	143	06	2	4	1/4	0/1

1) Number of donors yielding a positive response/total tested.
2) -- indicates binding affinity =10,000nM.

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Table XXVIII. Crossbinding of A2 supermotif analogs

			-	energie .					Annual Section
	:		SEQ ID	A*0201	A*0202	A*0203	A*0206	A*6802	No. A2
Source	AA	Sequence	NO:	иМ	Mu	Mu	nM	Mu	Alleles Crossbound
p53.69	∞	AAPPVAPA	1411	5000	1536	1177	1233	4706	0
p53.69L2V8	∞	ALPPVAPV	1412	217	7167	200	285	29	4
p53.101	11	KTYQGSYGFRL	1413	1786	968	:	514	615	0
p53.101L2V1	11	KLYQGSYGFRV	1414	81	48	24	116	-	4
p53.129	6	ALNKMFCQL	1415	735	391	19	73	ŀ	3
p53.129V9	6	ALNKMFCQV	1416	75	165	7.7	15	i	4
p53.129B7V9	6	ALNKMFBQV	1417	192	391	23	49	:	4
p53.129	10	ALNKMFCQLA	1418	1316	1075	71	4625	1	1
p53.129V10	10	ALNKMFCQLV	1419	217	287	71	7400	-	3
p53.132	6	KMFCQLAKT	1420	333	33	18	106	:	4
p53.132V9	6	KMFCQLAKV	1421	33	8.4	7.7	15	;	4
p53.132B4V9	6	KMFBQLAKV	1422	125	13	9.1	37	8889	4
p53.132L2V9	6	KLFCQLAKV	1423	86	3.6	3.4	10	1270	4
p53.135	6	CQLAKTCPV	1424	208	43	143	06	ŧ	4
p53.135L2	6	CLLAKTCPV	1425	125	909	<i>L</i> 9	370	ŀ	3
p53.135B1B7	6	BQLAKTBPV	1426	102	7.1	15	<i>L</i> 9	;	4
p53.135B1L2I	6	BLLAKTBPV	1427	46	119	7.7	64		4
p53.139	6	KTCPVQLWV	1428	725	909	217	15	:	2
p53.139L2	6	KLCPVQLWV	1429	122	239	29	23	:	4
p53.139L2B3	6	KLBPVQLWV	1430	46	29	19	31	-	4
p53.149	6	STPPPGTRV	1431	606	1162	1031	:	129	-
p53.149M2	6	SMPPPGTRV	1432	172	215	13	425	<i>L</i> 99	4
p53.149L2	6	SLPPPGTRV	1433	122	226	13	9250	140	4
p53.164	6	KQSQHMTEV	1434	200	130	170	285	ł	4
p53.164L2	6	KLSQHMTEV	1435	122	94	35	46	į	4
p53.216	10	VVVPYEPPEV	1436	617	1870	455	1194	ł	_
p53.216L2	10	VLVPYEPPEV	1437	68	391	71	2056	1	3
p53.236	11	YMCNSSCMGGM	1438	<i>L</i> 99	391	<i>L</i> 9	974	5333	2
p53.236L2M1	11	YLCNSSCMGGV	1439	22	13	3.6	18	1569	4
p53.255	11	ITLEDSSGNLL	1440	1563	1265	2857	207	<i>L</i> 999	0
p53.255L2V1	11	ILLEDSSGNLV	1441	./. 33	123	71	206	1	4
			1						

⁻⁻ indicates binding affinity =10,000nM.

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	CTL Peptide ¹	CTL Wild-	CTL
p53.69	8	AAPPVAPA	1442	5000	1536	1177	1777	7007	CIOSSOOUIIG		type	
p53.691.2V8	œ	AT DDV/ A DV	1440		0001	1111	1233	4/00	0			
		ALLE VAL V	1443	/17	7167	500	285	<i>L</i> 9	4	2/4	1/3	0/3
p53.129	6	ALNKMFCŐL	1444	735	391	19	73	2 -	3			
p53.129V9	6	ALNKMFCQV	1445	75	165	7.7	5	:) <i>4</i>	7		
p53.129B7V9	6	ALNKMFBÖV	1446	192	391	23	40		t <	7/0	Ç	
p53.132	6	KMFCOLAKT	1447	333	33	2 2	101		1	7/4	0/3	0/2
p53.132V9	6	KMFCOLAKV	1448	33	, «	100	100	ł	4			
p53.132B4V9	0	KMEROI AKV	1440	3,5	t .	7.7	\mathbf{C}	;	4	1/3	0/2	0/2
n53 1321 2V9	٠ ٥	VACASCIANA	1449	C71	13	9.1	37	8888	4	5/5	0/4	0/4
252 120		NLFCQLAKV	1450	88	3.6	3.4	9.5	1270	4	2/3	1/3	۲/0
p55.139	ν.	KICPVQLWV	1451	725	909	217	15		2			
p53.139L2	6	KLCPVQLWV	1452	122	239	29	23	1	1 =	ýč	9	9
p53.139L2B3	6	KLBPVQLWV	1453	45	29	10	2 17	ł	† -	C/7	2/3	1/3
p53.149	6	STPPPGTRV	1454	006	1163	1021	21	: 6	4	3/4	2/3	1/2
p53.149L2	6	SLPPPGTRV	1455	122	2011	1201	: 0	671				
p53.149M2	6	SMPPPGTRV	1456	172	215	C 7	7250	140	4 ,	2/3	1/3	0/3
p53.216	10	VVVPYEPPEV	1457	617	1070	234	C7+	/00	4	2/4	2/4	2/4
053.2161.2	10	VI VPVEDDEV	1450) 0	16/0	455	1194	. !				1
n52 755	<u>}</u>	THE PROCESS	1430	8	391	71	2056	;	n	1/1	1/1	
p33.233	-	ITEDSSCIPE	1459	1563	1265	2857	507	6667	C			
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	}	> 4	1/3	0/3	c,
									-	2/1	2/2	7/0

¹⁾ Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity =10,000nM.

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Table XXX. DR supertype primary binding

	— <u></u>							
Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFRLGFLHSGTAKS	V 1461	P53.108	3	5.4	89	omding 2
39.0308	2	LNKMFCQLAKTCPV	0 1462	P53.130	20	804	167	2
39.0309	2	MGGMNRRPILTIITL	11	P53.243				0
39.0310	2	RRPILTIITLEDSSG	11	P53.248	5000	4500		0
39.0311	2	KRALPNNTSSSPOPK	11	P53.305				0
39.0312	2	DGEYFTLQIRGRERI	11	P53.324	125			1

⁻⁻ indicates binding affinity =10,000nM.

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Table XXXI. DR supertype cross-binding

	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 DR2w2 DR6w1 DR5w1 DR8w2 DR147 β1 nM β2 nM 9 nM 1 nM nM Binding	DR2w2 DR2w2 DR6w β1 nM β2 nM 9 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM		Broad Binding (5/8)
JFR.	GFRLGFLHSGTAKSV	1467	p53.108	2.6	5.4	68	253	167	92	100	29	3	∞
39.0308 LNK	NKMFCQLAKTCPV	1468	p53.130	20	804	167	5688	541	365	2500	1531	n	S

-- indicates binding affinity = 10,000nM.

Table XXX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFRLGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVÇ	1462	P53.130	20	804	167	3
39.0309	2	MGGMNRRPILTIITL	1463	P53.243				0
39.0310	2	RRPILTIITLEDSSG	1464	₽ ⁵ 53.248	5000	4500		0
39.0311	2	KRALPNNTSSSPQPK	1465	/P53.305				0
39.0312	2	DGEYFTLQIRGRERF	1466	/ P53.324	125			1

⁻⁻ indicates binding affinity =10,000nM.

1

1:00

DR 3 Binder	0	0
Broad Binding (5/8)	8	5
DR14 7 Bindin	3	3
DR8w 2 nM	56	1531
DR6w DR5w DR8w 1 1 2 9 nM 1 nM nM	100	2500
DR6w 1 9 nM	92	365
DR2w 2 β2 nM	167	541
DR2w 2 β1 nM	253	2688
DR3 nM		;
DR7 nM	68	167
DR4w 4 nM	5.4	804
DR1 nM	2.6	20
SEQ ID Source NO:	V 1485p53.108	Q 1486p53.130
Sequence	39.0307 GFRLGFLHSGTAKSV 1485p53.108	39.0308 LNKMFCQLAKTCPVQ 1486 653.130
Peptide	9.0307	9.0308

-- indicates binding affinity = 10,000nM.